



OIIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/977,577

DATE: 02/08/2002
 TIME: 13:59:40

Input Set : A:\MOESTRUP1A.txt
 Output Set: N:\CRF3\02082002\I977577.raw

P.S.

3 <110> APPLICANT: MOESTRUP, Soren
 4 MOLLER, Holger J.
 6 <120> TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR AND THE
 USES THEREOF

8 <130> FILE REFERENCE: MOESTRUP=1A
 10 <140> CURRENT APPLICATION NUMBER: 09/977,577
 11 <141> CURRENT FILING DATE: 2001-10-16
 13 <150> PRIOR APPLICATION NUMBER: US 60/270,120
 14 <151> PRIOR FILING DATE: 2001-02-22
 16 <150> PRIOR APPLICATION NUMBER: DK PA 2001 00039
 17 <151> PRIOR FILING DATE: 2001-01-11
 19 <150> PRIOR APPLICATION NUMBER: DK PA 2000 01543
 20 <151> PRIOR FILING DATE: 2000-10-16
 22 <160> NUMBER OF SEQ ID NOS: 25
 24 <170> SOFTWARE: PatentIn version 3.1

ENTERED

26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 347
 28 <212> TYPE: PRT
 29 <213> ORGANISM: Homo sapiens
 31 <400> SEQUENCE: 1
 33 Met Ser Ala Leu Gly Ala Val Ile Ala Leu Leu Leu Trp Gly Gln Leu
 34 1 5 10 15
 37 Phe Ala Val Asp Ser Gly Asn Asp Val Thr Asp Ile Ala Asp Asp Gly
 38 20 25 30
 41 Cys Pro Lys Pro Pro Glu Ile Ala His Gly Tyr Val Glu His Ser Val
 42 35 40 45
 45 Arg Tyr Gln Cys Lys Asn Tyr Tyr Lys Leu Arg Thr Glu Gly Asp Gly
 46 50 55 60
 49 Val Tyr Thr Leu Asn Asn Glu Lys Gln Trp Ile Asn Lys Ala Val Gly
 50 65 70 75 80
 53 Asp Lys Leu Pro Glu Cys Glu Ala Val Cys Gly Lys Pro Lys Asn Pro
 54 85 90 95
 57 Ala Asn Pro Val Gln Arg Ile Leu Gly Gly His Leu Asp Ala Lys Gly
 58 100 105 110
 61 Ser Phe Pro Trp Gln Ala Lys Met Val Ser His His Asn Leu Thr Thr
 62 115 120 125
 65 Gly Ala Thr Leu Ile Asn Glu Gln Trp Leu Leu Thr Thr Ala Lys Asn
 66 130 135 140
 69 Leu Phe Leu Asn His Ser Glu Asn Ala Thr Ala Lys Asp Ile Ala Pro
 70 145 150 155 160
 73 Thr Leu Thr Leu Tyr Val Gly Lys Lys Gln Leu Val Glu Ile Glu Lys
 74 165 170 175
 77 Val Val Leu His Pro Asn Tyr Ser Gln Val Asp Ile Gly Leu Ile Lys
 78 180 185 190

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81 Leu Lys Gln Lys Val Ser Val Asn Glu Arg Val Met Pro Ile Cys Leu
82      195      200      205
85 Pro Ser Lys Asp Tyr Ala Glu Val Gly Arg Val Gly Tyr Val Ser Gly
86      210      215      220
89 Trp Gly Arg Asn Ala Asn Phe Lys Phe Thr Asp His Leu Lys Tyr Val
90 225      230      235      240
93 Met Leu Pro Val Ala Asp Gln Asp Gln Cys Ile Arg His Tyr Glu Gly
94      245      250      255
97 Ser Thr Val Pro Glu Lys Lys Thr Pro Lys Ser Pro Val Gly Val Gln
98      260      265      270
101 Pro Ile Leu Asn Glu His Thr Phe Cys Ala Gly Met Ser Lys Tyr Gln
102      275      280      285
105 Glu Asp Thr Cys Tyr Gly Asp Ala Gly Ser Ala Phe Ala Val His Asp
106      290      295      300
109 Leu Glu Glu Asp Thr Trp Tyr Ala Thr Gly Ile Leu Ser Phe Asp Lys
110 305      310      315      320
113 Ser Cys Ala Val Ala Glu Tyr Gly Val Tyr Val Lys Val Thr Ser Ile
114      325      330      335
117 Gln Asp Trp Val Gln Lys Thr Ile Ala Glu Asn
118      340      345
121 <210> SEQ ID NO: 2
122 <211> LENGTH: 406
123 <212> TYPE: PRT
124 <213> ORGANISM: Homo sapiens
126 <400> SEQUENCE: 2
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132 Phe Ala Val Asp Ser Gly Asn Asp Val Thr Asp Ile Ala Asp Asp Gly
133      20      25      30
136 Cys Pro Lys Pro Pro Glu Ile Ala His Gly Tyr Val Glu His Ser Val
137      35      40      45
140 Arg Tyr Gln Cys Lys Asn Tyr Tyr Lys Leu Arg Thr Glu Gly Asp Gly
141      50      55      60
144 Val Tyr Thr Leu Asn Asp Lys Lys Gln Trp Ile Asn Lys Ala Val Gly
145 65      70      75      80
148 Asp Lys Leu Pro Glu Cys Glu Ala Asp Asp Gly Cys Pro Lys Pro Pro
149      85      90      95
152 Glu Ile Ala His Gly Tyr Val Glu His Ser Val Arg Tyr Gln Cys Lys
153      100      105      110
156 Asn Tyr Tyr Lys Leu Arg Thr Glu Gly Asp Gly Val Tyr Thr Leu Asn
157      115      120      125
160 Asn Glu Lys Gln Trp Ile Asn Lys Ala Val Gly Asp Lys Leu Pro Glu
161      130      135      140
164 Cys Glu Ala Val Cys Gly Lys Pro Lys Asn Pro Ala Asn Pro Val Gln
165 145      150      155      160
168 Arg Ile Leu Gly Gly His Leu Asp Ala Lys Gly Ser Phe Pro Trp Gln
169      165      170      175
172 Ala Lys Met Val Ser His His Asn Leu Thr Thr Gly Ala Thr Leu Ile
173      180      185      190

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176 Asn Glu Gln Trp Leu Leu Thr Thr Ala Lys Asn Leu Phe Leu Asn His
177      195      200      205
180 Ser Glu Asn Ala Thr Ala Lys Asp Ile Ala Pro Thr Leu Thr Leu Tyr
181      210      215      220
184 Val Gly Lys Lys Gln Leu Val Glu Ile Glu Lys Val Val Leu His Pro
185 225      230      235      240
188 Asn Tyr Ser Gln Val Asp Ile Gly Leu Ile Lys Leu Lys Gln Lys Val
189      245      250      255
192 Ser Val Asn Glu Arg Val Met Pro Ile Cys Leu Pro Ser Lys Asp Tyr
193      260      265      270
196 Ala Glu Val Gly Arg Val Gly Tyr Val Ser Gly Trp Gly Arg Asn Ala
197      275      280      285
200 Asn Phe Lys Phe Thr Asp His Leu Lys Tyr Val Met Leu Pro Val Ala
201      290      295      300
204 Asp Gln Asp Gln Cys Ile Arg His Tyr Glu Gly Ser Thr Val Pro Glu
205 305      310      315      320
208 Lys Lys Thr Pro Lys Ser Pro Val Gly Val Gln Pro Ile Leu Asn Glu
209      325      330      335
212 His Thr Phe Cys Ala Gly Met Ser Lys Tyr Gln Glu Asp Thr Cys Tyr
213      340      345      350
216 Gly Asp Ala Gly Ser Ala Phe Ala Val His Asp Leu Glu Glu Asp Thr
217      355      360      365
220 Trp Tyr Ala Thr Gly Ile Leu Ser Phe Asp Lys Ser Cys Ala Val Ala
221      370      375      380
224 Glu Tyr Gly Val Tyr Val Lys Val Thr Ser Ile Gln Asp Trp Val Gln
225 385      390      395      400
228 Lys Thr Ile Ala Glu Asn
229      405
232 <210> SEQ ID NO: 3
233 <211> LENGTH: 347
234 <212> TYPE: PRT
235 <213> ORGANISM: Ateles geoffroyi
237 <400> SEQUENCE: 3
239 Met Ser Ala Leu Gly Ala Val Ile Ala Leu Leu Leu Trp Gly Gln Leu
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243 Phe Ala Val Asp Ser Gly Asn Asp Val Thr Asp Ile Ala Asp Asp Gly
244      20      25      30
247 Cys Pro Lys Pro Pro Glu Ile Ala Asn Gly Tyr Val Glu His Leu Val
248      35      40      45
251 Arg Tyr Gln Cys Lys Lys Tyr Tyr Arg Leu Arg Thr Glu Gly Asp Gly
252      50      55      60
255 Val Tyr Thr Leu Asn Asn Glu Lys Gln Trp Thr Asn Lys Ala Val Gly
256 65      70      75      80
259 Asp Lys Leu Pro Glu Cys Glu Ala Val Cys Gly Lys Pro Lys Asn Pro
260      85      90      95
263 Ala Asn Pro Val Gln Arg Ile Leu Gly Gly His Leu Asp Ala Lys Gly
264      100      105      110
267 Ser Phe Pro Trp Gln Ala Lys Met Val Ser Arg His Asn Leu Thr Thr
268      115      120      125

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271 Gly Ala Thr Leu Ile Asn Glu Gln Trp Leu Leu Thr Thr Ala Lys Asn
272      130      135      140
275 Leu Phe Leu Asn His Ser Glu Asn Ala Thr Ala Lys Asp Ile Ala Pro
276 145      150      155      160
279 Thr Leu Thr Leu Tyr Val Gly Lys Asn Gln Leu Val Glu Ile Glu Lys
280      165      170      175
283 Val Val Leu Tyr Pro Asn Tyr Ser Gln Val Asp Ile Gly Leu Ile Lys
284      180      185      190
287 Leu Lys Asp Lys Val Pro Val Asn Glu Arg Val Met Pro Ile Cys Leu
288      195      200      205
291 Pro Ser Lys Asp Tyr Ala Glu Val Gly Arg Val Gly Tyr Val Ser Gly
292      210      215      220
295 Trp Gly Arg Asn Ala Asn Phe Lys Phe Thr Asp His Leu Lys Tyr Val
296 225      230      235      240
299 Met Leu Pro Val Ala Asp Gln Tyr Gln Cys Val Lys His Tyr Glu Gly
300      245      250      255
303 Ser Thr Val Pro Glu Lys Lys Thr Pro Lys Ser Pro Val Gly Gln Gln
304      260      265      270
307 Pro Ile Leu Asn Glu His Thr Phe Cys Ala Gly Met Ser Lys Tyr Gln
308      275      280      285
311 Glu Asp Thr Cys Tyr Gly Asp Ala Gly Ser Ala Phe Ala Val His Asp
312      290      295      300
315 Leu Glu Glu Asp Thr Trp Tyr Ala Ala Gly Ile Leu Ser Phe Asp Lys
316 305      310      315      320
319 Ser Cys Gly Val Ala Glu Tyr Gly Val Tyr Val Lys Ala Thr Ser Ile
320      325      330      335
323 Gln Asp Trp Val Gln Lys Thr Ile Ala Glu Asn
324      340      345
327 <210> SEQ ID NO: 4
328 <211> LENGTH: 347
329 <212> TYPE: PRT
330 <213> ORGANISM: Mus caroli
332 <400> SEQUENCE: 4
334 Met Arg Ala Leu Gly Ala Val Val Thr Leu Leu Leu Trp Gly Gln Leu
335 1      5      10      15
338 Phe Ala Val Glu Leu Gly Asn Asp Ala Met Asp Phe Glu Asp Asp Ser
339      20      25      30
342 Cys Pro Lys Pro Pro Glu Ile Ala Asn Gly Tyr Val Glu His Leu Val
343      35      40      45
346 Arg Tyr Arg Cys Arg Gln Phe Tyr Arg Leu Arg Ala Glu Gly Asp Gly
347      50      55      60
350 Val Tyr Thr Leu Asn Asp Glu Lys Gln Trp Met Asn Thr Val Ala Gly
351 65      70      75      80
354 Glu Lys Leu Pro Glu Cys Glu Ala Val Cys Gly Lys Pro Lys His Pro
355      85      90      95
358 Val Asp Gln Val Gln Arg Ile Ile Gly Gly Ser Met Asp Ala Lys Gly
359      100      105      110
362 Ser Phe Pro Trp Gln Ala Lys Met Ile Ser Arg His Gly Leu Thr Thr
363      115      120      125

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```

366 Gly Ala Thr Leu Ile Ser Asp Gln Trp Leu Leu Thr Thr Ala Lys Asn
367      130      135      140
370 Leu Phe Leu Asn His Ser Glu Thr Ala Ser Gly Lys Asp Ile Ala Pro
371 145      150      155      160
374 Thr Leu Thr Leu Tyr Val Gly Lys Asn Gln Leu Val Glu Ile Glu Lys
375      165      170      175
378 Val Ile Leu His Pro Asn His Ser Val Val Asp Ile Gly Leu Ile Lys
379      180      185      190
382 Leu Lys Gln Arg Val Leu Val Thr Glu Arg Val Met Pro Ile Cys Leu
383      195      200      205
386 Pro Ser Lys Asp Tyr Val Ala Pro Gly Arg Val Gly Tyr Val Ser Gly
387      210      215      220
390 Trp Gly Arg Asn Gln Asp Phe Arg Phe Thr Asp Arg Leu Lys Tyr Val
391 225      230      235      240
394 Met Leu Pro Val Ala Asp Gln Asp Lys Cys Val Val His Tyr Glu Lys
395      245      250      255
398 Ser Thr Val Pro Glu Lys Lys Asn Phe Thr Ser Pro Val Gly Val Gln
399      260      265      270
402 Pro Ile Leu Asn Glu His Thr Phe Cys Ala Gly Leu Thr Lys Tyr Glu
403      275      280      285
406 Glu Asp Thr Cys Tyr Gly Asp Ala Gly Ser Ala Phe Ala Ile His Asp
407      290      295      300
410 Met Glu Glu Asp Thr Trp Tyr Ala Ala Gly Ile Leu Ser Phe Asp Lys
411 305      310      315      320
414 Ser Cys Ala Val Ala Glu Tyr Gly Val Tyr Val Arg Ala Thr Asp Leu
415      325      330      335
418 Lys Asp Trp Val Gln Glu Thr Met Ala Lys Asn
419      340      345
422 <210> SEQ ID NO: 5
423 <211> LENGTH: 347
424 <212> TYPE: PRT
425 <213> ORGANISM: Mus musculus
427 <400> SEQUENCE: 5
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430 1      5      10      15
433 Phe Ala Val Glu Leu Gly Asn Asp Ala Met Asp Phe Glu Asp Asp Ser
434      20      25      30
437 Cys Pro Lys Pro Pro Glu Ile Ala Asn Gly Tyr Val Glu His Leu Val
438      35      40      45
441 Arg Tyr Arg Cys Arg Gln Phe Tyr Arg Leu Arg Ala Glu Gly Asp Gly
442      50      55      60
445 Val Tyr Thr Leu Asn Asp Glu Lys Gln Trp Val Asn Thr Val Ala Gly
446 65      70      75      80
449 Glu Lys Leu Pro Glu Cys Glu Ala Val Cys Gly Lys Pro Lys His Pro
450      85      90      95
453 Val Asp Gln Val Gln Arg Ile Ile Gly Gly Ser Met Asp Ala Lys Gly
454      100      105      110
457 Ser Phe Pro Trp Gln Ala Lys Met Ile Ser Arg His Gly Leu Thr Thr
458      115      120      125

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/977,577

DATE: 02/08/2002

TIME: 13:59:41

Input Set : A:\MOESTRUP1A.txt

Output Set: N:\CRF3\02082002\I977577.raw

L:606 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:2417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21